pseudopeptide containing at least one amino acid addition, deletion, or substitution in the amino acid sequence.

5. (Amended) The inhibitor molecule according to any one of claims 2 to 4 in which a -CONH- peptide bond is replaced by a ($-CH_2NH-$) reduced bond, a (-NHCO-) retro inverso bond, a ($-CH_2-O-$) methylene-oxy bond, a ($-CH_2-S-$) thiomethylene bond, a ($-CH_2CH_2-$) carba bond, a ($-CO-CH_2-$) cetomethylene bond, a ($-CHOH-CH_2-$) hydroxyethylene bond, a (-N-N-) bond, a E-alcene bond, or a (-CH=CH-) bond.

6. (Amended) The inhibitor molecule according to any one of claims 2 to 5, which comprises amino acid sequences selected from the following P95/nucleolin sequences:

- the sequence beginning at the amino acid in position 22 and ending at the amino acid in position 44 of SEQ ID NO: 1;

- the sequence beginning at the amino acid in position 143 and ending at the amino acid in position 171 of SEQ ID NO: 1;

- the sequence beginning at the amino acid in position 185 and ending at the amino acid in position 209 of SEQ ID NO: 1; and

- the sequence beginning at the amino acid in position 234 and ending at the amino acid in position 271 of SEQ ID NO: 1.

9. (Amended) An inhibitor molecule, which comprises a polymer of an inhibitor molecule according to any one of claims 3 to 6, that contains 2 to 20 monomer units from the amino acid sequence of P95/nucleolin, P40/PHAPIII, or P30/PHAPI.

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10. (Amended) The inhibitor molecule according to any one of claims 2 to 6 or 9, which is a MAP matrix structure.

13. (Amended) A therapeutic composition comprising a pharmaceutically effective amount of an inhibitor molecule according to any one of claims 2 to 6 or 9 to 10, optionally in combination with another anti-HIV molecule.

23. (Amended) A method for screening an inhibitor according to any one of claims 2 to 6, 9 to 10, 13, or 22, comprising:

a) bringing into contact at least one cell expressing an HIV receptor at its surface with an amount of a HIV retrovirus equal to the $TCID_{50}$;

b) incubating said at least one cell and retroviruses at 37°C during a period of time sufficient to allow the entry of the retrovirus within the at least one cell, in the presence of a defined amount of the compound to be assayed;

c) washing the at least one cell in order to remove the retroviruses that have been absorbed onto the membranes of the at least one cell;

d) treating the at least one cell in order to eliminate the remaining extracellular retroviruses by a controlled proteolysis with trypsin;

e) preparing cytoplasmic extracts by treating the at least one cell of step d) with an extraction buffer containing 20 mM Tris-HCl (pH7.6), 0.15 M NaCl, 5 mM $MgCl_2$, 0.2 mM PMSF, 100 U/ml aprotinin and 0.5% Triton X-100;

f) centrifuging the at least one cell obtained at step c), at 1000 g, and harvesting the supernatant medium, in order to separate the retroviral proteins; and

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